

Fig. 19 A

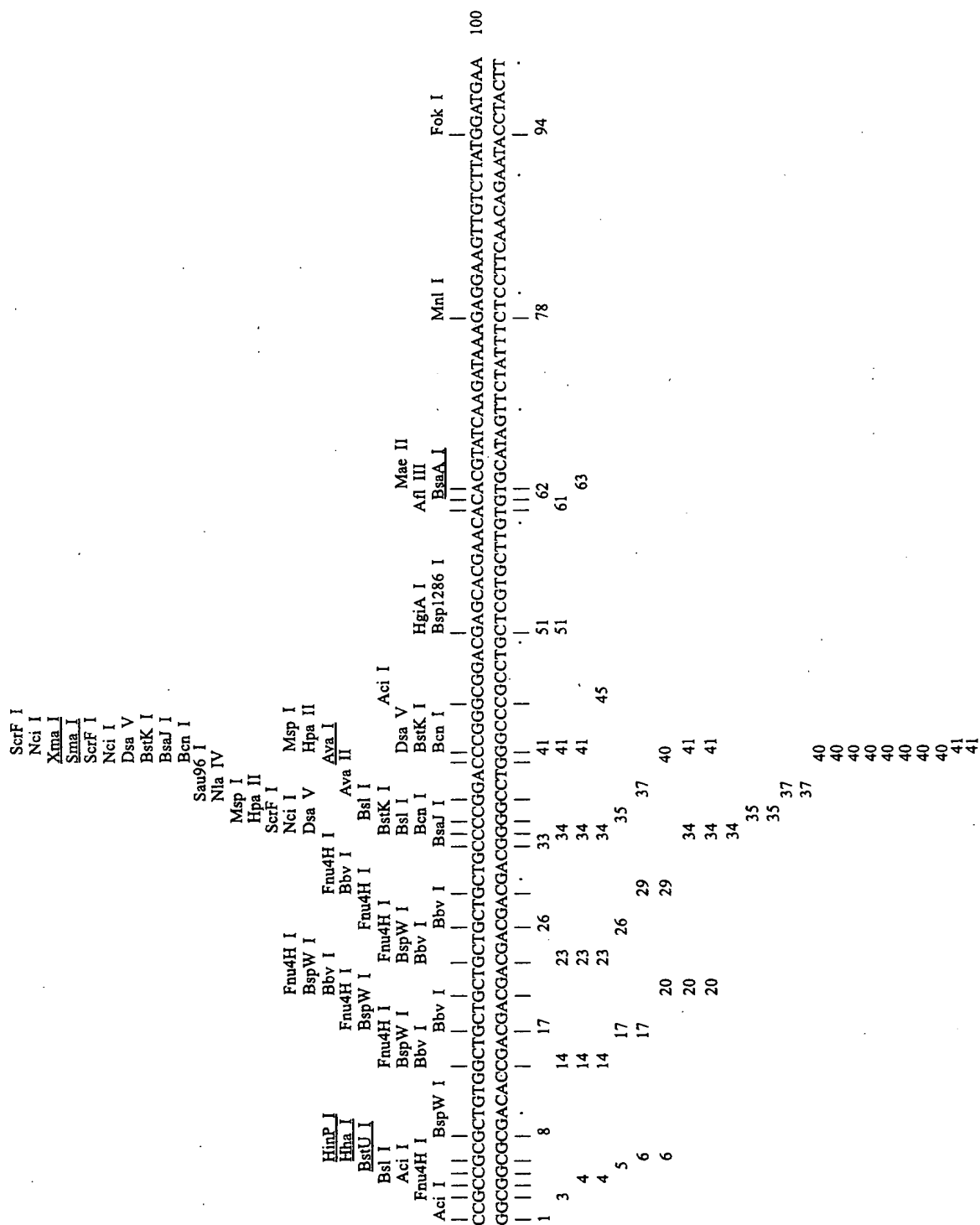


Fig. 19 B

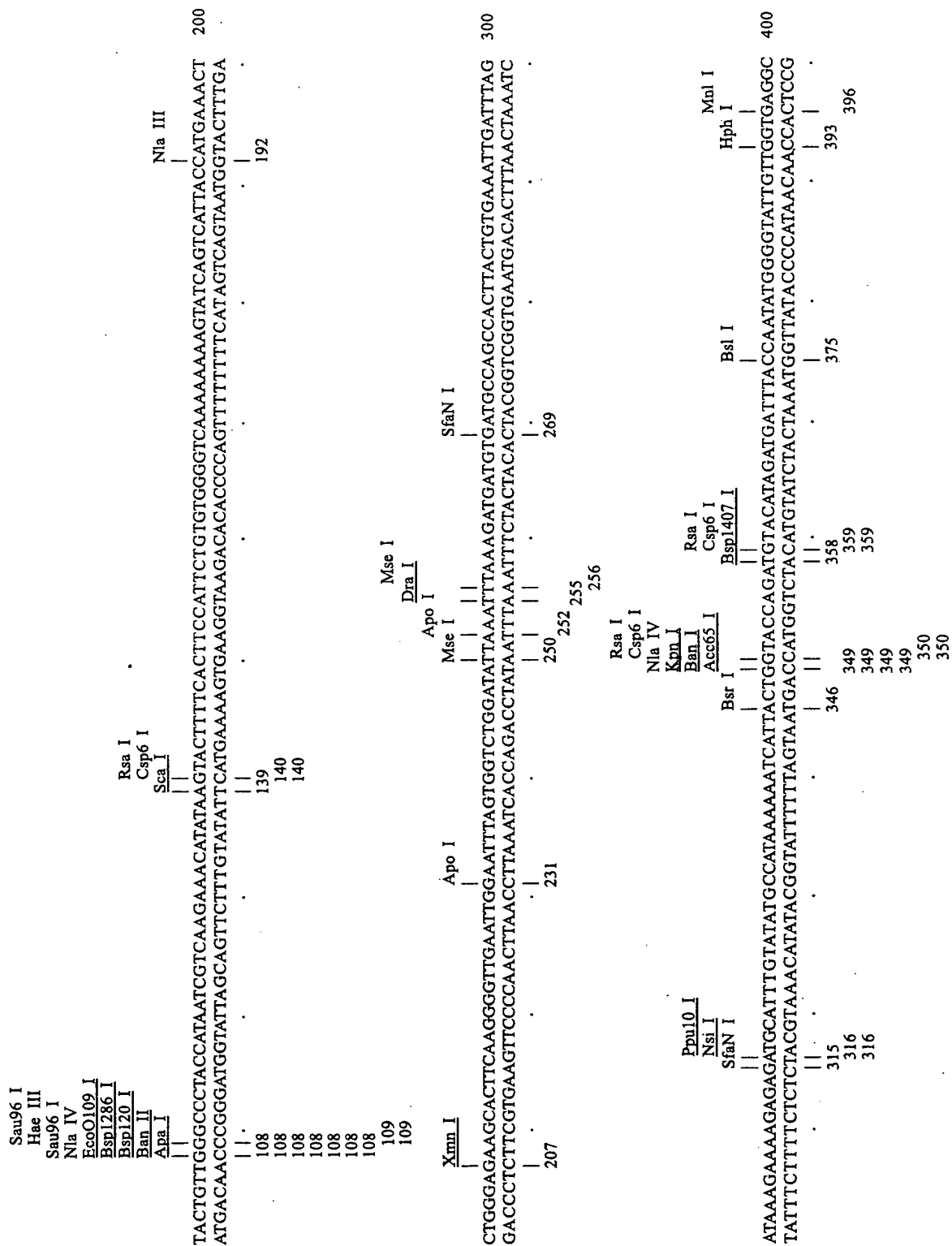


Fig. 19 C

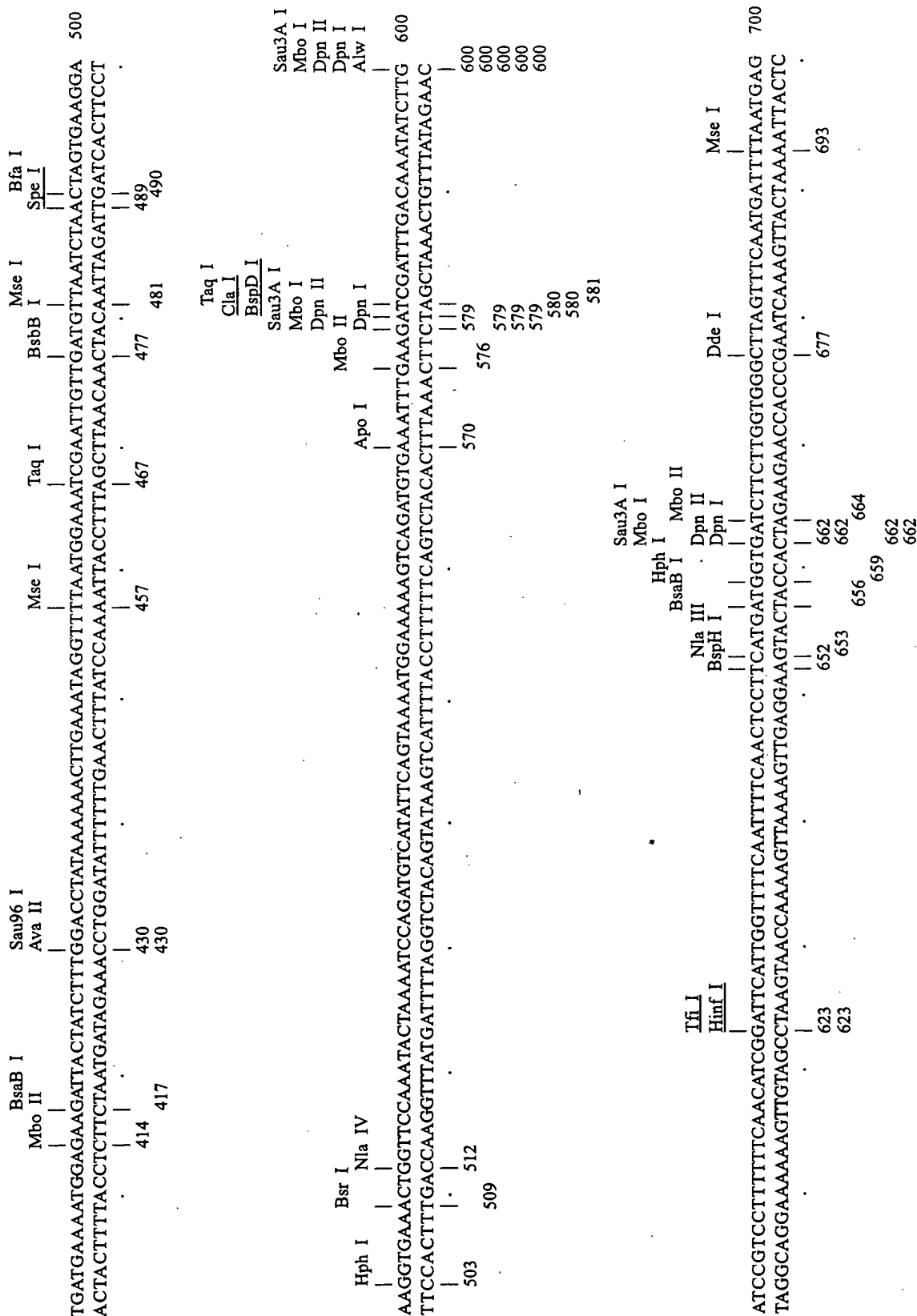


Fig. 19D

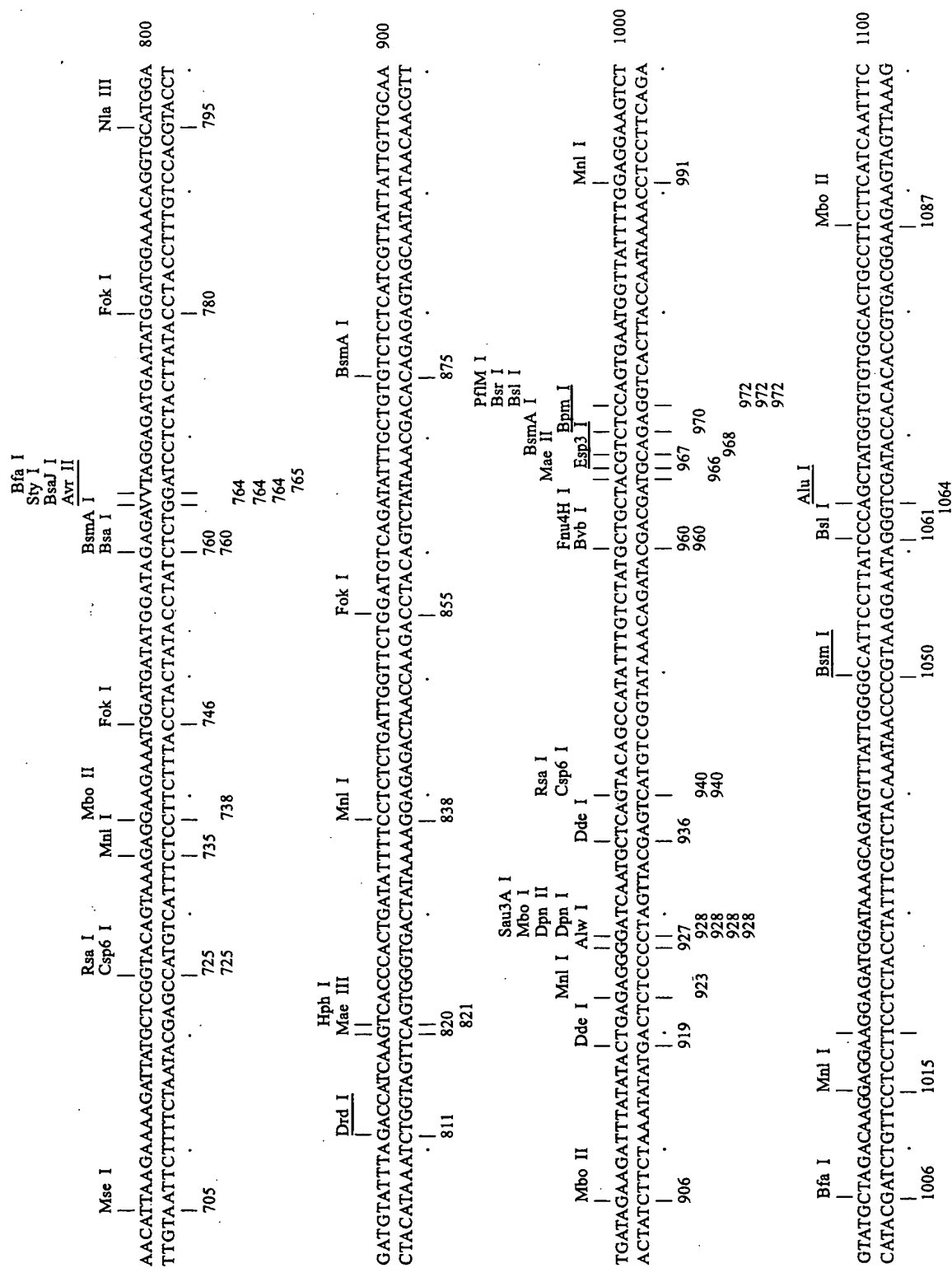


Fig. 19 E

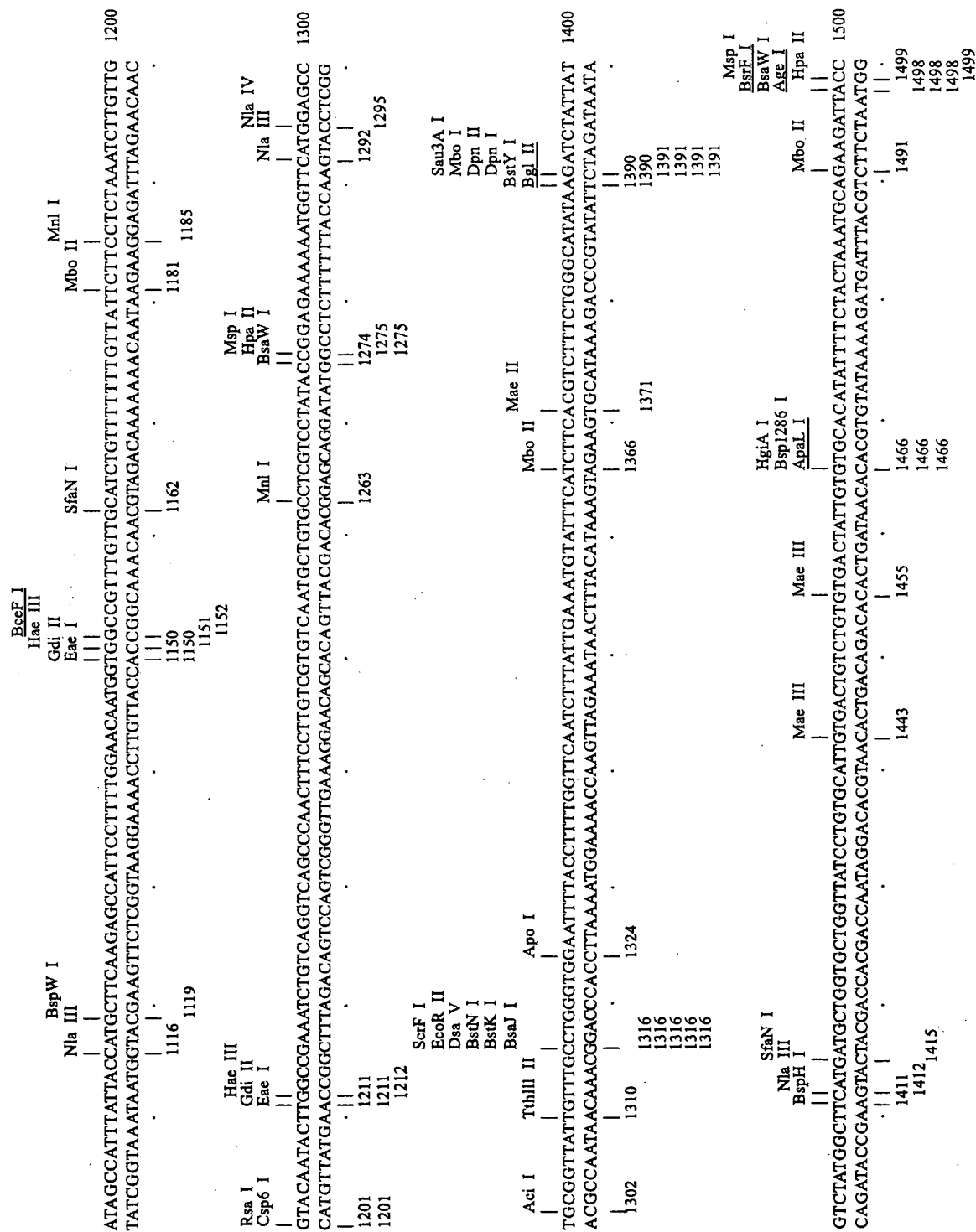


Fig. 19 F

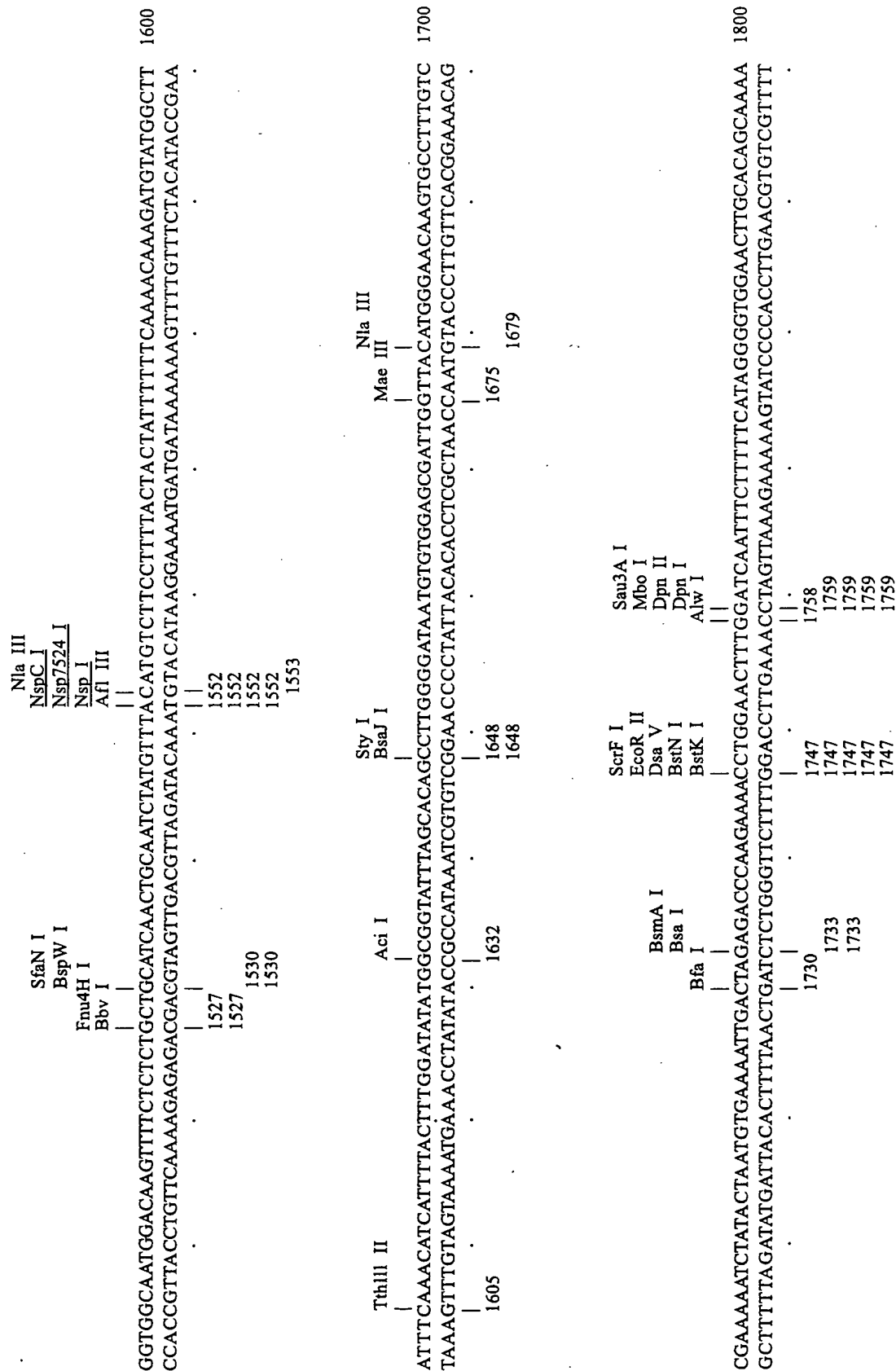


Fig. 22 A

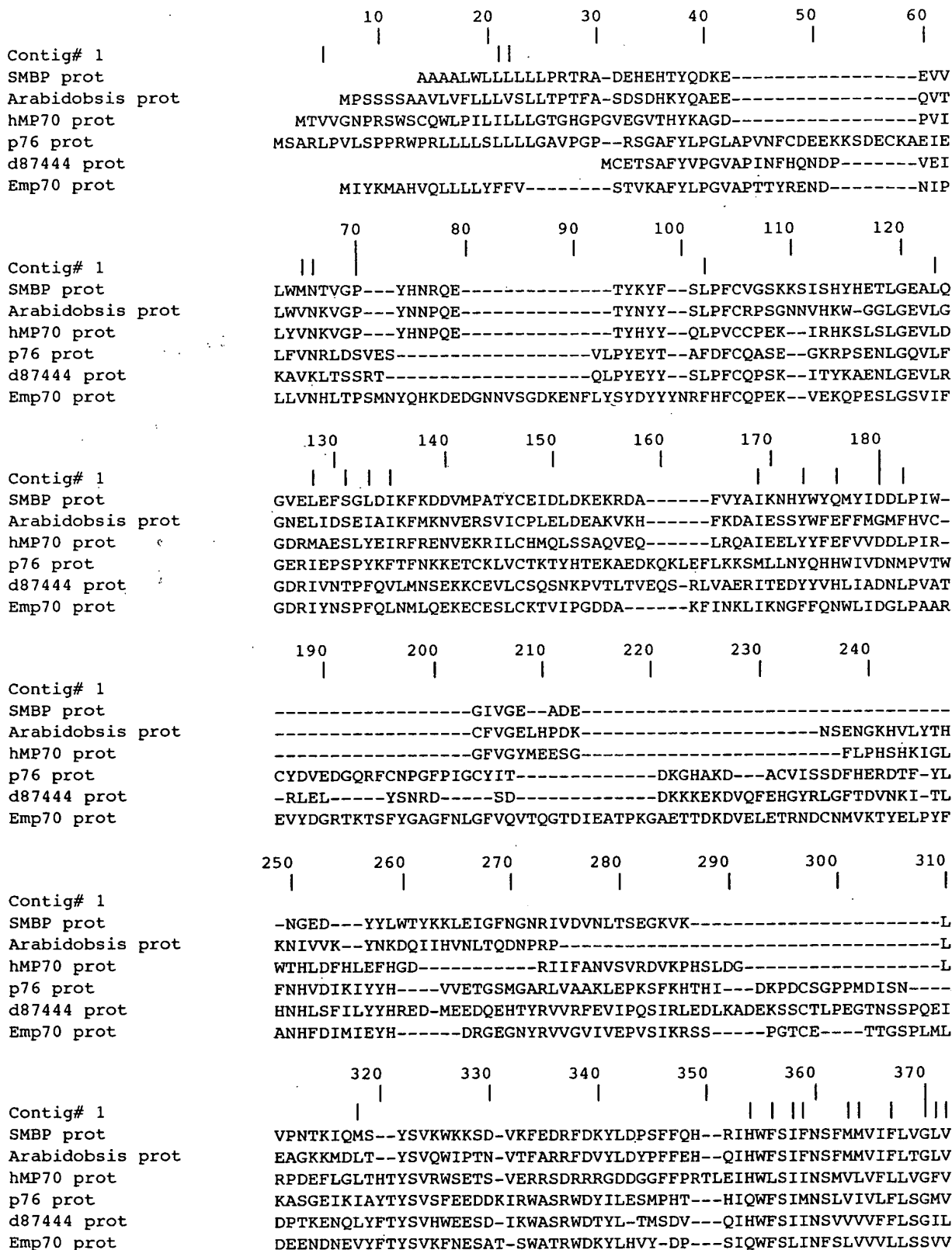


Fig. 22 B

	380	390	400	410	420	430
Contig# 1						
SMBP prot	SMILMRTLKRDYARTSKEEE-MDD-MDRDLGD-EYGWKQVHGDVFRPSSHPLIFSSSLIGSGC					
Arabidopsis prot	SMILMRTLRLNDYAKYAREDDDDLES-LERDVSE-ESGWKLHGDVFRPASSLVLLSAVVGTTGA					
hMP70 prot	AVILMRVLRNDLARYNLDEETTSAGSGDDFDQGDNGWKIHTDVFRPPYRGLLCAVLGVGA					
p76 prot	AMIMLRTLHKDIARYNQ-----MDSTED-AQEEFGWKLHGDIFRPPRKGMLLSVFLGSGT					
d87444 prot	SMIIIRTLRKDIANYNK-----EDDIED-TMEESGWKLHGDVFRPPQYOMILSSLLGSGI					
Emp70 prot	IHSLLRALKSDFARYNE-----LNLDDD-FQEDSGWKLNHGDVFRSPSLSLTLILVSGSV					

	440	450	460	470	480	490
Contig# 1						
SMBP prot	QIFAVSLIIVIAMIEDLYTER-GSMLSTAIFVYAATSPVNGYFGGSLYARQGGRRWIKQMF					
Arabidopsis prot	QLALLVLLVILMAIVGTLYVGR-GAIVTTFIVCYALTSFVSGYVSGGMYSRSGGKHWHKCMV					
hMP70 prot	QFLALGTGIIVMALLGMFNVHRHGAINSAAILLYALTCCISGYVSSHFYRQIGGERWVWNII					
p76 prot	QILIMTFVTLFFACLGLSPANRGALMTCVAVLVLLGTPAGYVAARFYKSFGGEKWKTNVL					
d87444 prot	QLFCMILIVIFVAMLGMLSPSSRGALMTTACFLFMFMGVFGGFSAGRLYRTLKGHRWKKGAF					
Emp70 prot	QLFLMVTCSIFFAALGLFLSPSSRGSLATVMFILYALFGFVGSYTSMDGIYKFFNGPYWKANLI					

	500	510	520	530	540	550
Contig# 1						
SMBP prot	IGAFLIPAMVCGTAFFINFIAIYYHASRAIPFGTMVAVCCICFFVILPLNLVGTILGRNLSG					
Arabidopsis prot	LTASLFPFLCFGIGFLNTIAIFYGSLAAIPFGTMVVVFVIWGFISFPLALLGTVGRNWSG					
hMP70 prot	LTTSLSFVPPFLTWSVNVSVHWANGSTQALPATITLLLTWVLLVGFPLTVIGGIFGKNNAS					
p76 prot	LTSFLCPGIVFADFFIMNLILWEGEGSSAAIPFGTLVAILALWFCISVPLTFFIGAYFGFKK-N					
d87444 prot	CTATLYPGVVFGICFVLNCFIWGKHSSGAVPFPPTMALLCMWFGISLPLVYLGYFYFGRK-Q					
Emp70 prot	LTPLLVPGAILLIIIALNFFLMFVHSSGVIPASTLFFMVFLWLFLFSIPSSFAGSLIARKRCH					

	560	570	580	590	600	610	620
Contig# 1							
SMBP prot	QPNFPCRVNAVPRPIPEKKWFMEPAVIVCLGGILPFGSIFIEMYFIFTSFWAYKIYYVYGFM						
Arabidopsis prot	APNNPCRVTIPRPIPEKKWYLTSPSVVSLMGGLLPFGSIFIEMYFVFTSFWNYKVYYVYGFM						
hMP70 prot	PFDAPCRTKNIAREINQPYKSTDIHMTVGGFLPFSASIVELYIIFATVWGREQTYLGIL						
p76 prot	AIEHPVRTNQIPRQIEQSIFYTKPLPGIIMGGILPFGCIFIQLFFILNSIWSHQMYMFGFL						
d87444 prot	PYDNPVRTNQIPRQIEQRWYMNRFVGIIMAGILPFGAMFIELFFIFSAIWENQFYFLFGFL						
Emp70 prot	WDEHPTKTNQIARQIPQPYWLKTIPATLIAGIFPFGSIAVELYFIYTSLWFNKIFYMFGFL						

	630	640	650	660	670	680
Contig# 1						
SMBP prot	MLVLVILCIVTVCTIVCTYFLLNAEDYRWQWTSFSLAASST-AIYVYMYSFYYYFFKTKMYG					
Arabidopsis prot	LLVFVILVIVTVCTIVGTIYFLLNAENYHWQWTSFFSAASST-AVYVYLYSIYYYVYVTKMSG					
hMP70 prot	FFVFAILLVSGASISIALTYFQLSGEDYRWWRVSVLSVGST-GLFIFLYSVFYARSRNMSG					
p76 prot	FLVFIIILVITCSEATILLCYFHLCAEDYHWQWRSFLTSGFT-AVYFLIYAVHYFFSKLQITG					
d87444 prot	FLVFIIILVVSQSIIVMVYFQLCAEDYRWWRNFLVSGGS-AFYVLVYAIIFYVFNKLDIVE					
Emp70 prot	FFSFLLLTLTSSLVTILITYHSLCLENWKWQWRGFIIGGAGCALYVFIHSILF--TKFKLGG					

	690	700	710	720
Contig# 1				
SMBP prot	LFQTSFYFGYMAVFSALGIMCGAIGYMGTSAFVRKIYTNVKID			
Arabidopsis prot	FFQTSFYFGYTMFCLGLGILCGAVGYLGSNLFVRRIYRNKCD			
hMP70 prot	AVQTVEFFGYSLLTGYVFFLMLGTISFFSSLKFIIRIYYVNLKMD			
p76 prot	TASTILYFGYTMIMVLIFFLFTGTIGFFACFWVTKIYSVVKVD			
d87444 prot	FIPSLLYFGYTALMVLVSFLLTGTIGFYAAYMFVRKIYAAYKID			
Emp70 prot	FTTIVLYVGYSSVISLLCCLVTGSIGFISSMLFVRKIYSSIKVD			

Fig. 23 A

Hydropathy index (Kyte-Doolittle, 1982)

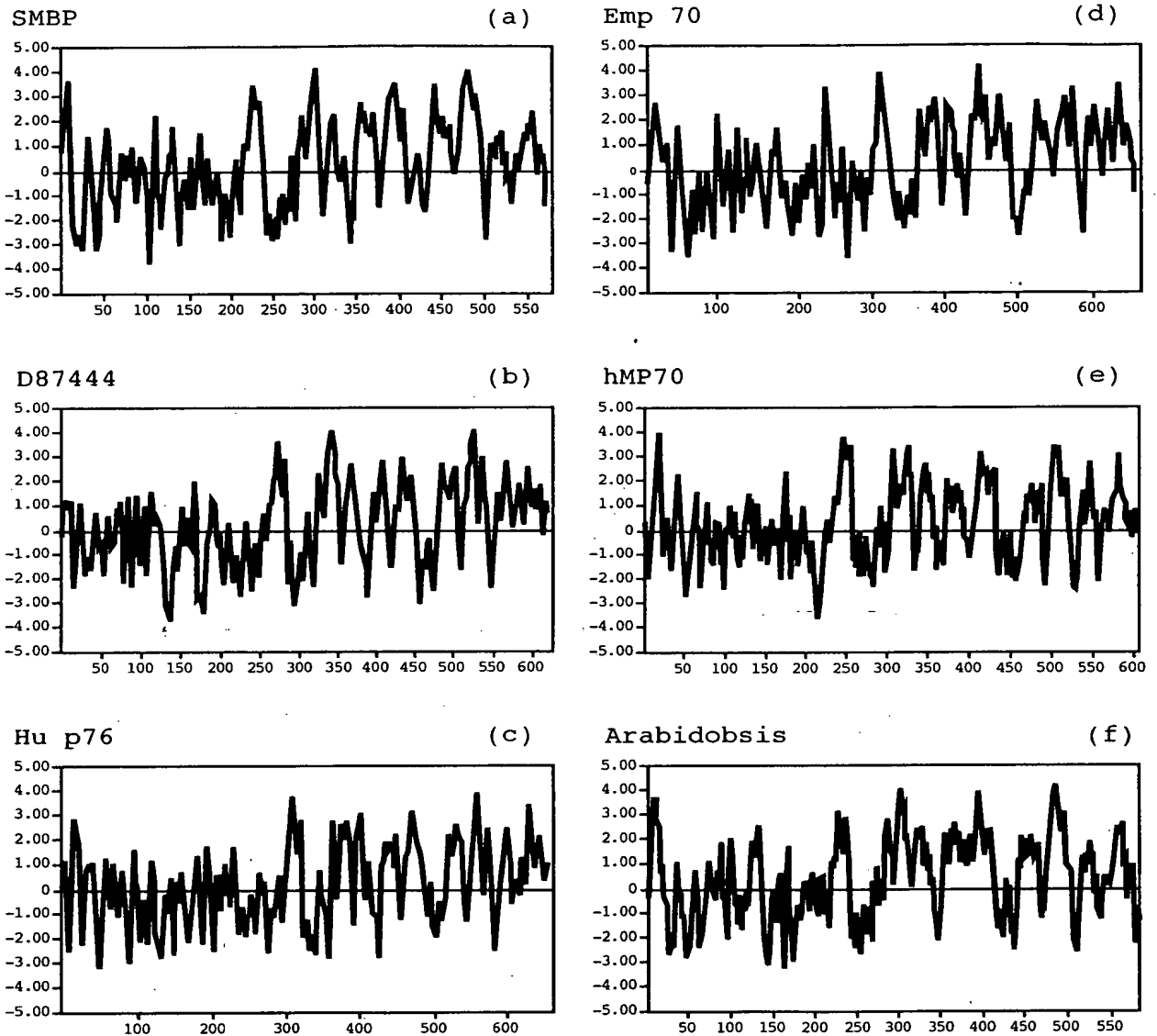


Fig. 23 B

Hydropathy index (Kyte-Doolittle, 1982)

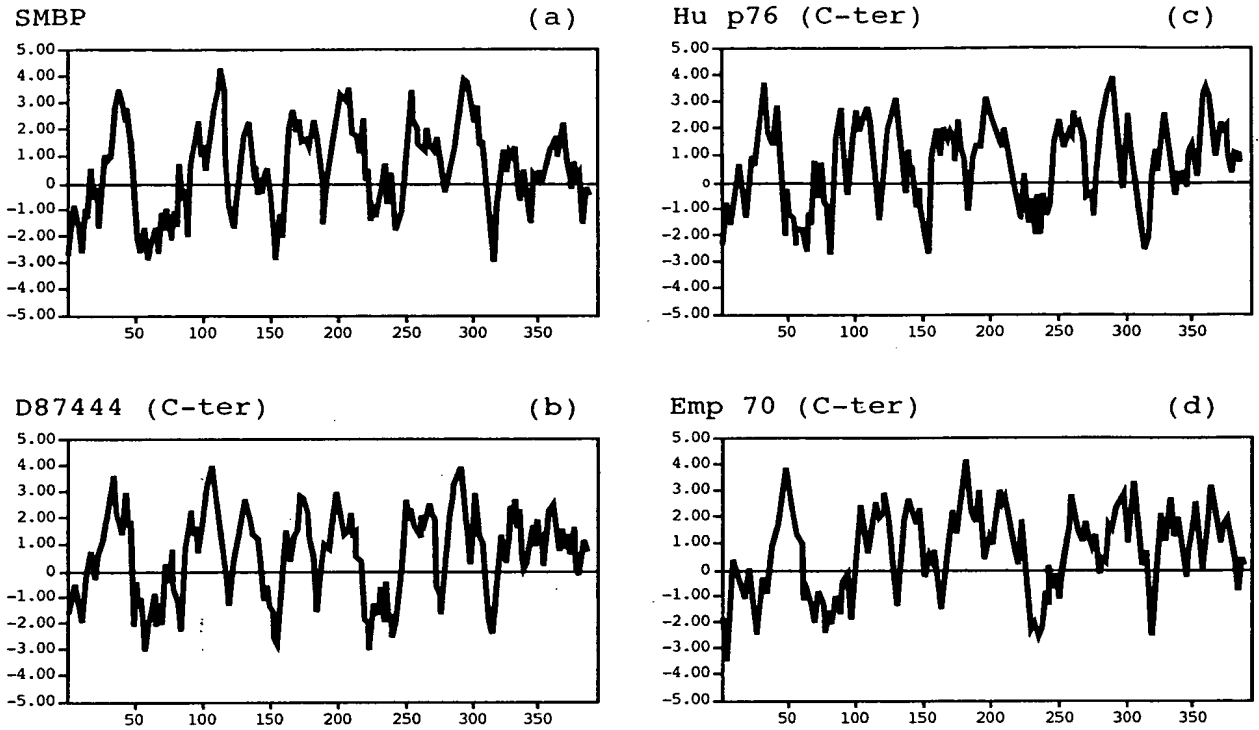


Fig. 24 A

1	CC GCC GCG CTG TGG CTG CTG CTG CTG CTG CCC CGG ACC CGG GCG GAC GAG CAC GAA CAC ACG TAT CAA GAT	74
1	A A L W L L L L L L L P R T R A D E H E H T Y Q D	24
75	AAA GAG GAA GTT GTC TTA TGG ATG AAT ACT GTT GGG CCC TAC CAT AAT CGT CAA GAA ACA TAT CCG TAC TTT TCA CTT CCA TTC TGT GTG	164
25	K E E V V L W M N T V G P Y H N R Q E T Y K Y F S L P F C V	54
165	GGG TCA AAA AAA AGT ATC AGT CAT TAC CAT GAA ACT CTG GGA GAA GCA CTT CAA GGG GTT GAA TTG GAA TTT AGT GGT CTG GAT ATT AAA	254
55	G S K K S I S H Y H E T L G E A L Q G V E L E F S G L D I K	84
255	TTT AAA GAT GAT GTG ATG CCA GCC ACT TAC TGT GAA ATT GAT TTA GAT AAA GAA AAG AGA GAT GCA TTT GTA TAT CCC ATA AAA AAT CAT	344
85	F K D D V M P A T Y C E I D L D K E K R D A F V Y A I K N H	114
345	TAC TGG TAC CAG ATG TAC ATA GAT GAT TTA CCA ATA TGG GGT ATT GTT GGT GAG GCT GAT GAA AAT GGA GAA GAT TAC TAT CTT TGG ACC	434
115	Y W Y Q M Y I D D L P I W G I V G E A D E N G E D Y Y L W T	144
435	TAT AAA AAA CTT GAA ATA GGT TTT AAT GGA AAT CGA ATT GTT GAT GTT AAT CTA ACT AGT GAA GGA AAG GTG AAA CTG CTT CCA AAT ACT	524
145	Y K K L E I G F N G N R I V D V N L T S E G K V K L V P N T	174
525	AAA ATC CAG ATG TCA TAT TCA GTA AAA TGG AAA AAC TCA GAT GTG AAA TTT GAA GAT CGA TTT GAC AAA TAT CTT GAT CCG TCC TTT TTT	614
175	K I Q M S Y S V K W K K S D V K F E D R F D K Y L D P S F F	204
615	CAA CAT CGG ATT CAT TGG TTT TCA ATT TTC AAC TCC TTC ATG ATG GTG ATC TTC TTG GTG GGC TTA GTT TCA ATG ATT TTA ATG AGA ACA	704
205	Q E R I H W F S I F N S F M M V I F L V G L V S M I L M R T	234
705	TTA AGA AAA GAT TAT GCT CGG TAC AGT AAA GAG GAA GAA ATG GAT GAT ATG GAT AGA GAC CTA GGA GAT GAA TAT GGA TGG AAA CAG GTG	794
235	L R K D Y A R Y S K E E E M D D M D R D L G D E Y G W K Q V	264
795	CAT GGA GAT GTA TTT AGA CCA TCA AGT CAC CCA CTG ATA TTT TCC TCT CTG ATT GGT TCT GGA TGT CAG ATA TTT GCT GTG TCT CTC ATC	884
265	H G D V F R P S S H P L I F S S L I G S G C Q I F A V S L I	294
885	GTT ATT ATT GTT GCA ATG ATA GAA GAT TTA TAT ACT GAG ACG GGA TCA ATG CTC AGT ACA GCC ATA TTT GTG TAT GCT GCT ACG TCT CCA	974
295	V I I V A M I E D L Y T E R G S M L S T A I F V Y A A T S P	324
975	GTG AAT GGT TAT TTT GGA GGA AGT CTG TAT GCT AGA CAA GGA GGA AGG AGA TGG ATA AAG CAG ATG TTT ATT GGG GCA TTC CTT ATC CCA	1064
325	V N G Y F G G S L Y A R Q G G R R W I K Q M F I G A F L I P	354
1065	CCT ATG GTG TGT GGC ACT GCC TTC TTC ATC AAT TTC ATA GCC ATT TAT TAC CAT GCT TCA AGA GCC ATT CCT TTT GGA ACA ATG GTG GCC	1154
355	A M V C G T A F F I N F I A I Y Y H A S R A I P F G T M V A	384
1155	GTT TGT TGC ATC TGT TTT TTT GTT ATT CTT CCT CTA AAT CTT GTT GGT ACA ATA CTT GGC CGA AAT CTG TCA GGT CAG CCC AAC TTT CCT	1244
385	V C C I C F F V I L P L N L V G T I L G R N L S G Q P N F P	414
1245	TGT GGT GTC AAT GCT GTG CCT CGT CCT ATA CCG GAG AAA AAA TGG TTC ATG GAG CCT GCG GTT ATT GTT TGC CTG GGT GGA ATT TTA CCT	1334
415	C R V N A V P R P I P E K K W F M E P A V I V C L G G I L P	444
1335	TTT GGT TCA ATC TTT ATT GAA ATG TAT TTC ATC TTC ACG TCT TTC TGG GCA TAT AAG ATC TAT TAT GTC TAT GGC TTC ATG ATG CTG GTG	1424
445	F G S I F I E M Y F I F T S F W A Y K I Y Y V Y G F M M L V	474
1425	CTG GTT ATC CTG TGC ATT GTG ACT GTC TGT GTG ACT ATT GTG TGC ACA TAT TTT CTA CTA AAT GCA GAA GAT TAC CGG TGG CAA TGG ACA	1514
475	L V I L C I V T V C V T I V C T Y F L L N A E D Y R W Q W T	504
1515	AGT TTT CTC TCT GCT GCA TCA ACT GCA ATC TAT GTT TAC ATG TAT TCC TTT TAC TAC TAT TTT TTC AAA ACA AAG ATG TAT GGC TTA TTT	1604
505	S F L S A A S T A I Y V Y M Y S F Y Y Y F F K T K M Y G L F	534
1605	CAA ACA TCA TTT TAC TTT GGA TAT ATG CCG GTA TTT AGC ACA GCC TTG GGG ATA ATG TGT GGA GCG ATT GGT TAC ATG GGA ACA AGT TTT	1694
535	Q T S F Y F G Y M A V F S T A L G I M C G A I G Y M G T S A	564
1695	TTT GTC CGA AAA ATC TAT ACT AAT CTG AAA ATT GAC TAG AGACCAAGAAAACCTGGAACCTTGGATCAATTCTTTTCATAGGGTGAACCTGCACAGCAAAA	1800
565	F V R K I Y T N V K I D	576

Fig. 24 B

